



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/784,553B  
Source: OIPB  
Date Processed by STIC: 4-17-03

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
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Revised 01/29/2002

Does Not Comply  
Corrected Diskette Needed



OIPF

## RAW SEQUENCE LISTING

DATE: 04/17/2003

PATENT APPLICATION: US/09/784,553B

TIME: 09:27:41

Input Set : A:\2459-1-003 CIP SeqList.txt

Output Set: N:\CRF4\04172003\I784553B.raw

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2 <110> APPLICANT: Zhou, Ming-Ming
3   Aggarwal, Aneel
5 <120> TITLE OF INVENTION: Methods of Identifying Modulators of Bromodomains
7 <130> FILE REFERENCE: 2459-1-003CIP
9 <140> CURRENT APPLICATION NUMBER: 09/784,553B
10 <141> CURRENT FILING DATE: 2001-02-16
12 <150> PRIOR APPLICATION NUMBER: 09/510,314
13 <151> PRIOR FILING DATE: 2000-02-22
15 <160> NUMBER OF SEQ ID NOS: 60
17 <170> SOFTWARE: PatentIn version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 3014
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
25 <400> SEQUENCE: 1
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27 gaggcctggca gccgccggca cgcacaccta gtccgcagtc ccgaggaaca tgtccgcagc      120
28 cagggcgcgag agcagagtcc cgggcaggag aaccaagga gggcgtgtgc tgtggcgcg      180
29 gccgcagcgg cagcggagcc gctagtcccc tccctcctgg gggagcagct gccgccgctg      240
30 ccgccgcgcg caccaccatc agcgcgcggg gcccgccag agcagcggcg gcgagcggcg      300
31 cgctaggggg agggcggggg cggggagggg ggtgggcgaa gggggcgggg gggcgtgggg      360
32 ggagggtctc gctctccga ctaccagagc ccgagggaga ccctggcggc gccggcgggcg      420
33 cctgacactc ggcgcctcct gccgtgctcc ggggcggcat gtccgaggct gccggggccg      480
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35 agcctgcggc gcttccgccc gcgccccgcg agggctcccc ctgcgcccgt gccgccgggg      600
36 gctcggggcg ctgcgggtcc gcgacggcag tggctgcagc gggcacggcc gaaggaccgg      660
37 gaggcggtgg ctcgcccgga atcgccgtga agaaagcgca actacgctcc gtcgccgggg      720
38 ccaagaaact ggagaaactc ggagtgtact ccgcctgcaa ggccgaggag tcttgtaaat      780
39 gtaatggctg gaaaaaccct aaccctcac ccaactcccc cagagccgac ctgcagcaaa      840
40 taattgtcag tctaacagaa tcctgtcgga gttgtagcca tgccctagct gtcctggttt      900
41 cccacctgga gaatgtgtca gaggaagaaa tgaacagact cctgggaata gtattggatg      960
42 tggaaatatc ttttacctgt gtccacaagg aagaagatgc agataccaaa caagtttatt      1020
43 tctatctatt taagctcttg agaaagtcta ttttacaagg aggaaaacct gtggttgaag      1080
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45 ttgtgcagta caaathtagt cacctgccag caaaagaaag gcaaacaata gttgagttgg      1200
46 caaaaatgtt cctaaaccgc atcaactatt ggcattctgga ggcaccatct caacgaagac      1260
47 tgcgatctcc caatgatgat atttctggat acaaagagaa ctacacaagg tggctgtgtt      1320
48 actgcaacgt gccacagttc tgcgacagtc tacctcggtc cgaaaccaca caggtgtttg      1380
49 ggagaacatt gcttcgctcg gtcttctact ttatgaggcg acaactcctg gaacaagcaa      1440
50 gacaggaaaa agataaactg cctcttgaaa aacgaactct aatcctcact catttcccaa      1500
51 aatttctgtc catgctagaa gaagaagtat atagtcaaaa ctctcccatc tgggatcagg      1560
52 attttctctc agcctcttcc agaaccagcc agctaggcat ccaaacagtt atcaatccac      1620
53 ctctgtggcg tgggacaatt tcatacaatt caacctcatc ttcccttgag cagccaaacg      1680

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54 cagggagcag cagtcctgcc tgcaaagcct cttctggact tgaggcaaac ccaggagaaa 1740
55 agaggaaaat gactgattct catgttctgg aggaggccaa gaaaccccga gttatggggg 1800
56 atattccgat ggaattaatc aacgaggtta tgtctacat caccgaccct gcagcaatgc 1860
57 ttggaccaga gaccaatttt ctgtcagcac actcggccag ggatgaggcg gcaaggttgg 1920
58 aagagcgagc ggggtgtaatt gaatttcacg tggttggcaa ttccctcaac cagaaaccaa 1980
59 acaagaagat cctgatgtgg ctggttgccc tacagaacgt tttctccac cagctgcccc 2040
60 gaatgcaaaa agaatacatc acacggctcg tctttgacct gaaacacaaa acccttgctt 2100
61 taattaaaga tggcctgtgt attggtggtt tctgtttccg tatgttccca tctcaaggat 2160
62 tcacagagat tgtcttctgt gctgtaacct caaatgagca agtcaagggc tatggaacac 2220
63 acctgatgaa tcatttgaaa gaatatcaca taaagcatga catcctgaac ttctcacat 2280
64 atgcagatga atatgcaatt ggatacttta agaaacaggg tttctccaaa gaaattaaaa 2340
65 tacctaaaac caaatatgtt ggctatatca aggattatga aggagccact ttaatgggat 2400
66 gtgagctaaa tccacggatc ccgtacacag aattttctgt catcattaaa aagcagaagg 2460
67 agataattaa aaaactgatt gaaagaaaac aggcacaaat tcgaaaagtt taccctggac 2520
68 tttcatgttt taaagatgga gttcgacaga ttcctataga aagcattcct ggaattagag 2580
69 agacaggctg gaaaccgagt ggaaaagaga aaagtaaaga gccagagac cctgaccagc 2640
70 tttacagcac gctcaagagc atcctccagc aggtgaagag ccatcaaagc gcttggccct 2700
71 tcatggaacc tgtgaagaga acagaagctc caggatatta tgaagttata aggttcccca 2760
72 tggatctgaa aaccatgagt gaacgcctca agaataggta ctacgtgtct aagaaattat 2820
73 tcatggcaga cttacagcga gtctttacca attgcaaaga gtacaacgcc gctgagagt 2880
74 aatactacaa atgtgccaat atcctggaga aattcttctt cagtaaaatt aaggaagctg 2940
75 gattaattga caagtgttt tttttcccc tctgcttctt agaaactcac caagcagtgt 3000
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78 &lt;210&gt; SEQ ID NO: 2

79 &lt;211&gt; LENGTH: 832

80 &lt;212&gt; TYPE: PRT

81 &lt;213&gt; ORGANISM: Homo sapiens

83 &lt;400&gt; SEQUENCE: 2

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85 Met Ser Glu Ala Gly Gly Ala Gly Pro Gly Gly Cys Gly Ala Gly Ala
86 1 5 10 15
88 Gly Ala Gly Ala Gly Pro Gly Ala Leu Pro Pro Gln Pro Ala Ala Leu
89 20 25 30
91 Pro Pro Ala Pro Pro Gln Gly Ser Pro Cys Ala Ala Ala Gly Gly
92 35 40 45
94 Ser Gly Ala Cys Gly Pro Ala Thr Ala Val Ala Ala Gly Thr Ala
95 50 55 60
97 Glu Gly Pro Gly Gly Gly Ser Ala Arg Ile Ala Val Lys Lys Ala
98 65 70 75 80
100 Gln Leu Arg Ser Ala Pro Arg Ala Lys Lys Leu Glu Lys Leu Gly Val
101 85 90 95
103 Tyr Ser Ala Cys Lys Ala Glu Glu Ser Cys Lys Cys Asn Gly Trp Lys
104 100 105 110
106 Asn Pro Asn Pro Ser Pro Thr Pro Pro Arg Ala Asp Leu Gln Gln Ile
107 115 120 125
109 Ile Val Ser Leu Thr Glu Ser Cys Arg Ser Cys Ser His Ala Leu Ala
110 130 135 140
112 Ala His Val Ser His Leu Glu Asn Val Ser Glu Glu Glu Met Asn Arg
113 145 150 155 160
115 Leu Leu Gly Ile Val Leu Asp Val Glu Tyr Leu Phe Thr Cys Val His

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116				165				170				175				
118	Lys	Glu	Glu	Asp	Ala	Asp	Thr	Lys	Gln	Val	Tyr	Phe	Tyr	Leu	Phe	Lys
119				180				185				190				
121	Leu	Leu	Arg	Lys	Ser	Ile	Leu	Gln	Arg	Gly	Lys	Pro	Val	Val	Glu	Gly
122				195				200				205				
124	Ser	Leu	Glu	Lys	Lys	Pro	Pro	Phe	Glu	Lys	Pro	Ser	Ile	Glu	Gln	Gly
125		210					215				220					
127	Val	Asn	Asn	Phe	Val	Gln	Tyr	Lys	Phe	Ser	His	Leu	Pro	Ala	Lys	Glu
128	225					230					235				240	
130	Arg	Gln	Thr	Ile	Val	Glu	Leu	Ala	Lys	Met	Phe	Leu	Asn	Arg	Ile	Asn
131				245				250				255				
133	Tyr	Trp	His	Leu	Glu	Ala	Pro	Ser	Gln	Arg	Arg	Leu	Arg	Ser	Pro	Asn
134				260				265				270				
136	Asp	Asp	Ile	Ser	Gly	Tyr	Lys	Glu	Asn	Tyr	Thr	Arg	Trp	Leu	Cys	Tyr
137			275					280				285				
139	Cys	Asn	Val	Pro	Gln	Phe	Cys	Asp	Ser	Leu	Pro	Arg	Tyr	Glu	Thr	Thr
140		290					295				300					
142	Gln	Val	Phe	Gly	Arg	Thr	Leu	Leu	Arg	Ser	Val	Phe	Thr	Val	Met	Arg
143	305					310					315				320	
145	Arg	Gln	Leu	Leu	Glu	Gln	Ala	Arg	Gln	Glu	Lys	Asp	Lys	Leu	Pro	Leu
146				325				330				335				
148	Glu	Lys	Arg	Thr	Leu	Ile	Leu	Thr	His	Phe	Pro	Lys	Phe	Leu	Ser	Met
149				340				345				350				
151	Leu	Glu	Glu	Glu	Val	Tyr	Ser	Gln	Asn	Ser	Pro	Ile	Trp	Asp	Gln	Asp
152			355					360				365				
154	Phe	Leu	Ser	Ala	Ser	Ser	Arg	Thr	Ser	Gln	Leu	Gly	Ile	Gln	Thr	Val
155		370					375				380					
157	Ile	Asn	Pro	Pro	Pro	Val	Ala	Gly	Thr	Ile	Ser	Tyr	Asn	Ser	Thr	Ser
158	385					390					395				400	
160	Ser	Ser	Leu	Glu	Gln	Pro	Asn	Ala	Gly	Ser	Ser	Ser	Pro	Ala	Cys	Lys
161				405				410				415				
163	Ala	Ser	Ser	Gly	Leu	Glu	Ala	Asn	Pro	Gly	Glu	Lys	Arg	Lys	Met	Thr
164				420				425				430				
166	Asp	Ser	His	Val	Leu	Glu	Glu	Ala	Lys	Lys	Pro	Arg	Val	Met	Gly	Asp
167			435					440				445				
169	Ile	Pro	Met	Glu	Leu	Ile	Asn	Glu	Val	Met	Ser	Thr	Ile	Thr	Asp	Pro
170		450					455					460				
172	Ala	Ala	Met	Leu	Gly	Pro	Glu	Thr	Asn	Phe	Leu	Ser	Ala	His	Ser	Ala
173	465					470					475				480	
175	Arg	Asp	Glu	Ala	Ala	Arg	Leu	Glu	Glu	Arg	Arg	Gly	Val	Ile	Glu	Phe
176				485				490				495				
178	His	Val	Val	Gly	Asn	Ser	Leu	Asn	Gln	Lys	Pro	Asn	Lys	Lys	Ile	Leu
179			500					505				510				
181	Met	Trp	Leu	Val	Gly	Leu	Gln	Asn	Val	Phe	Ser	His	Gln	Leu	Pro	Arg
182			515					520				525				
184	Met	Pro	Lys	Glu	Tyr	Ile	Thr	Arg	Leu	Val	Phe	Asp	Pro	Lys	His	Lys
185		530					535				540					
187	Thr	Leu	Ala	Leu	Ile	Lys	Asp	Gly	Arg	Val	Ile	Gly	Gly	Ile	Cys	Phe
188	545					550					555				560	

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190 Arg Met Phe Pro Ser Gln Gly Phe Thr Glu Ile Val Phe Cys Ala Val
191                               565                               570                               575
193 Thr Ser Asn Glu Gln Val Lys Gly Tyr Gly Thr His Leu Met Asn His
194                               580                               585                               590
196 Leu Lys Glu Tyr His Ile Lys His Asp Ile Leu Asn Phe Leu Thr Tyr
197                               595                               600                               605
199 Ala Asp Glu Tyr Ala Ile Gly Tyr Phe Lys Lys Gln Gly Phe Ser Lys
200                               610                               615                               620
202 Glu Ile Lys Ile Pro Lys Thr Lys Tyr Val Gly Tyr Ile Lys Asp Tyr
203 625                               630                               635                               640
205 Glu Gly Ala Thr Leu Met Gly Cys Glu Leu Asn Pro Arg Ile Pro Tyr
206                               645                               650                               655
208 Thr Glu Phe Ser Val Ile Ile Lys Lys Gln Lys Glu Ile Ile Lys Lys
209                               660                               665                               670
211 Leu Ile Glu Arg Lys Gln Ala Gln Ile Arg Lys Val Tyr Pro Gly Leu
212                               675                               680                               685
214 Ser Cys Phe Lys Asp Gly Val Arg Gln Ile Pro Ile Glu Ser Ile Pro
215                               690                               695                               700
217 Gly Ile Arg Glu Thr Gly Trp Lys Pro Ser Gly Lys Glu Lys Ser Lys
218 705                               710                               715                               720
220 Glu Pro Arg Asp Pro Asp Gln Leu Tyr Ser Thr Leu Lys Ser Ile Leu
221                               725                               730                               735
223 Gln Gln Val Lys Ser His Gln Ser Ala Trp Pro Phe Met Glu Pro Val
224                               740                               745                               750
226 Lys Arg Thr Glu Ala Pro Gly Tyr Tyr Glu Val Ile Arg Phe Pro Met
227                               755                               760                               765
229 Asp Leu Lys Thr Met Ser Glu Arg Leu Lys Asn Arg Tyr Tyr Val Ser
230                               770                               775                               780
232 Lys Lys Leu Phe Met Ala Asp Leu Gln Arg Val Phe Thr Asn Cys Lys
233 785                               790                               795                               800
235 Glu Tyr Asn Ala Ala Glu Ser Glu Tyr Tyr Lys Cys Ala Asn Ile Leu
236                               805                               810                               815
238 Glu Lys Phe Phe Phe Ser Lys Ile Lys Glu Ala Gly Leu Ile Asp Lys
239                               820                               825                               830

```

243 &lt;210&gt; SEQ ID NO: 3

244 &lt;211&gt; LENGTH: 16

245 &lt;212&gt; TYPE: PRT

246 &lt;213&gt; ORGANISM: Artificial Sequence

248 &lt;220&gt; FEATURE:

249 &lt;223&gt; OTHER INFORMATION: synthetic bromodomain peptide

251 &lt;220&gt; FEATURE:

W--&gt; 252 &lt;221&gt; NAME/KEY: Xaa

253 &lt;222&gt; LOCATION: (2)..(4)

254 &lt;223&gt; OTHER INFORMATION: Xaa is a maximum of three amino acids. Each of these can be any amino acid. One may be missing.

256 &lt;220&gt; FEATURE:

W--&gt; 257 &lt;221&gt; NAME/KEY: Xaa

258 &lt;222&gt; LOCATION: (4)..(11)

259 &lt;223&gt; OTHER INFORMATION: Xaa is a maximum of eight amino acids. Each of these can be any amino acid. One, two, or three may be missing.

262 &lt;220&gt; FEATURE:

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Input Set : A:\2459-1-003 CIP SeqList.txt

Output Set: N:\CRF4\04172003\I784553B.raw

W--> 263 <221> NAME/KEY: Xaa  
 264 <222> LOCATION: (5)..(5)  
 265 <223> OTHER INFORMATION: Xaa is a single amino acid that is either Pro, Lys, or His.  
 268 <220> FEATURE:

W--> 269 <221> NAME/KEY: Xaa  
 270 <222> LOCATION: (6)..(6)  
 271 <223> OTHER INFORMATION: Xaa is any single amino acid.  
 274 <220> FEATURE:

W--> 275 <221> NAME/KEY: Xaa  
 276 <222> LOCATION: (8)..(8)  
 277 <223> OTHER INFORMATION: Xaa is a single amino acid that can be either Tyr, Phe, or His.  
 280 <220> FEATURE:

W--> 281 <221> NAME/KEY: Xaa  
 282 <222> LOCATION: (9)..(13)  
 283 <223> OTHER INFORMATION: Xaa is 5 amino acids. Each of these can be any amino acid.  
 286 <220> FEATURE:

W--> 287 <221> NAME/KEY: Xaa  
 288 <222> LOCATION: (11)..(11)  
 289 <223> OTHER INFORMATION: Xaa is a single amino acid that can be either Met, Ile, or Val.  
 292 <400> SEQUENCE: 3

W--> 294 Phe Xaa Pro Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Asp  
 295 1 5 10 15  
 298 <210> SEQ ID NO: 4  
 299 <211> LENGTH: 12  
 300 <212> TYPE: PRT  
 301 <213> ORGANISM: Artificial Sequence

W--> 302 <220> FEATURE:  
 303 <223> OTHER INFORMATION: synthetic bromodomain peptide

W--> 306 <220> FEATURE:

W--> 307 <221> NAME/KEY: Xaa  
 308 <222> LOCATION: (6)..(6)  
 309 <223> OTHER INFORMATION: Xaa represents an acetyl-lysine  
 311 <400> SEQUENCE: 4

W--> 313 Ile Ser Tyr Gly Arg Xaa Lys Arg Arg Gln Arg Arg  
 314 1 5 10  
 316 <210> SEQ ID NO: 5  
 317 <211> LENGTH: 14  
 318 <212> TYPE: PRT  
 319 <213> ORGANISM: Artificial Sequence  
 321 <220> FEATURE:  
 322 <223> OTHER INFORMATION: synthetic bromodomain peptide  
 325 <220> FEATURE:

W--> 326 <221> NAME/KEY: Xaa  
 327 <222> LOCATION: (8)..(8)  
 328 <223> OTHER INFORMATION: Xaa represents an acetyl lysine.  
 330 <400> SEQUENCE: 5

W--> 332 Ala Arg Lys Ser Thr Gly Gly Xaa Ala Pro Arg Lys Gln Leu  
 333 1 5 10  
 336 <210> SEQ ID NO: 6

All Xaa must be  
 accounted for in  
 feature

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 2,4,5,6,8,9,10,11,12,13,15  
Seq#:4; Xaa Pos. 6  
Seq#:5; Xaa Pos. 8  
Seq#:6; Xaa Pos. 8  
Seq#:43; Xaa Pos. 1,2,4,6,7,8,10,11,12,13,14,15,17  
Seq#:46; Xaa Pos. 5  
Seq#:48; Xaa Pos. 2,4,6,8,10  
Seq#:50; Xaa Pos. 5  
Seq#:51; Xaa Pos. 5  
Seq#:52; Xaa Pos. 5  
Seq#:53; Xaa Pos. 5  
Seq#:54; Xaa Pos. 5  
Seq#:55; Xaa Pos. 5  
Seq#:56; Xaa Pos. 5  
Seq#:57; Xaa Pos. 6  
Seq#:58; Xaa Pos. 7  
Seq#:59; Xaa Pos. 16

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:3; Line(s) 254,259  
Seq#:34; Line(s) 1159  
Seq#:35; Line(s) 1188  
Seq#:43; Line(s) 1448,1453  
Seq#:46; Line(s) 1541  
Seq#:48; Line(s) 1572,1577,1582,1587

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/784,553B

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TIME: 09:27:42

Input Set : A:\2459-1-003 CIP SeqList.txt

Output Set: N:\CRF4\04172003\I784553B.raw

L:252 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:257 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:263 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:269 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:275 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:281 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:287 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0  
L:302 M:283 W: Missing Blank Line separator, <220> field identifier  
L:307 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4  
L:313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0  
L:326 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:332 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0  
L:346 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
L:352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0  
L:1436 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43  
L:1441 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43  
L:1446 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43  
L:1451 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43  
L:1456 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43  
L:1461 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43  
L:1466 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43  
L:1471 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43  
L:1476 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43  
L:1482 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0  
L:1539 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:46  
L:1545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0  
L:1570 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:48  
L:1575 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:48  
L:1580 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:48  
L:1585 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:48  
L:1590 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:48  
L:1596 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:0  
L:1630 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:50  
L:1636 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:0  
L:1648 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:51  
L:1654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0  
L:1666 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:52  
L:1672 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52 after pos.:0  
L:1684 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:53  
L:1690 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53 after pos.:0  
L:1702 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:54  
L:1708 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54 after pos.:0  
L:1720 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:55  
L:1726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55 after pos.:0  
L:1738 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:56  
L:1744 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:0  
L:1756 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:57



## VERIFICATION SUMMARY

DATE: 04/17/2003

PATENT APPLICATION: US/09/784,553B

TIME: 09:27:42

Input Set : A:\2459-1-003 CIP SeqList.txt

Output Set: N:\CRF4\04172003\I784553B.raw

L:1763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:0  
L:1775 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:58  
L:1781 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:0  
L:1794 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:59  
L:1800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59 after pos.:0